

GenCore version 5.1.4.p5.4578
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OM nucleic - protein search, using frame_plus.n2p model

Run on: May 7, 2003, 15:14:59 ; Search time 95 Seconds

(without alignments)
6581.666 Million cell updates/sec

Title: US-09-965-830-1-COPY_6_3257

Perfect score: 6089

Sequence: 1 atgcgcgcacatgcgagcct.....aagaagcagcagggctcga 3252

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE-frame+.n2p.model -DEV=xlp
-O/cgcn2.1/USPTO.spool/US09965830/rnat.07052003.151449.6267/app-query.fasta.1.3399
-DB-PIR-73 -OPMT-fastan -SUFFIX-PIR -MINMATCH-0.1 -LOOPCL-0 -LOOEXT-0
-UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR SCORE-pct -THR MAX-100 -THR MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-PRO -NORM-ext -HEADSITE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-us09965830.ecgn.1.1.163.0/rnat.07052003.151449.6267 -NCPD-6 -ICPD-3
-NO_XLPRX -NO_MAP -LARGEUDERY -NEG SCORES-0 -WAIT -LONGLOG -DEV-TIMEOUT-120
-WARN-TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
-XGAPOP-10 -YGAPEXT-0.5 -DELop-6 -DELEXT-7

Database:

PIR-73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query Match length DB ID

Description

1	5428	89.1	1087	2	T31100	
2	2515	41.3	1102	2	T17367	probable potassium
3	2439.5	40.1	1017	2	T31354	potassium channel
4	1901	31.2	1284	2	T13168	probable potassium
5	1551	25.5	1159	2	T13845	probable potassium
6	1390	22.8	1174	2	A40853	potassium channel
7	1380.5	22.7	962	2	I53197	potassium channel
8	1371.5	22.5	989	2	I48912	potassium channel
9	1257	20.6	934	2	T42394	potassium channel
10	1029.5	16.9	514	2	T19579	hypothetical prote
11	439	7.2	706	2	A55251	cyclic nucleotide-
12	423.5	6.9	735	2	I50630	alpha subunit of c
13	421.5	6.9	665	2	S52072	dmnGC protein - f
14	421.5	6.9	691	2	JC6509	rod cyclic nucleot

15	420	6.9	695	2	S74179	cyclic nucleotide-
16	416.5	6.8	732	2	S35691	cyclic nucleotide-
17	414.5	6.8	682	1	JH0560	cyclic nucleotide-
18	414	6.8	688	2	B42161	cAMP-gated cation
19	413.5	6.8	690	1	S07103	cAMP-gated ion cha
20	413	6.8	686	1	A44842	cAMP-gated ion cha
21	411	6.7	645	2	I50680	alpha subunit of r
22	407	6.7	690	2	A42161	cAMP-gated cation
23	401	6.6	641	1	S23809	cyclic nucleotide-
24	393	6.5	664	2	S11517	cAMP-gated channel
25	391.5	6.4	663	2	S11521	collagen alpha 1(I)
26	391	6.4	1453	2	S21626	collagen alpha 1(I)
27	389.5	6.4	1464	1	CGH015	collagen alpha 1(I)
28	386.5	6.3	787	2	S68699	collagen alpha 1(I)
29	371	6.1	3570	2	T45025	potassium channel
30	370	6.1	575	2	ICGH015	collagen alpha 1(I)
31	369.5	6.1	575	2	I59327	collagen alpha 1(I)
32	368.5	6.1	733	2	EB8357	collagen alpha 1(I)
33	367.5	6.0	1042	2	CGCH15	hypothetical prote
34	365	6.0	738	2	EB8294	hypothetical prote
35	361	5.9	880	2	F85381	probable potassium
36	361	5.9	916	2	T05360	hypothetical 119.5
37	361	5.9	1106	2	J00405	collagen alpha 1(I)
38	360	5.9	1453	2	S21626	collagen alpha 1(I)
39	358.5	5.9	1418	2	T45467	collagen alpha 1(I)
40	357	5.9	710	2	T52573	cyclic nucleotide
41	356.5	5.9	1486	1	B40333	collagen alpha 1(I)
42	356.5	5.9	1414	1	S23809	collagen alpha 2(I)
43	354.5	5.8	747	2	T52572	cyclic nucleotide
44	353.5	5.8	1806	1	CGH015	collagen alpha 1(X
45	352	5.8				

ALIGNMENTS

RESULT 1
T31100

probable potassium channel 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Oct-1999 #sequence-revision 22-Oct-1999 #text-change 22-Oct-1999

C:Accession: T31100

R:Engelard, B.; Neu, A.; Ludwig, J.; Roeper, J.; Pongs, O.
Submitted to the EMBL Data Library, July 1998

A:Description: Identification of three rat potassium channel genes homologous to D. m

A:Reference number: Z20983

A:Accession: T31100

A:Molecule type: mRNA

A:Residues: 1-1087 <ENG>

A:Cross-references: EMBL:AJ007627; NID:e1329995; PID:e1329996; PID:CA07586.1

A:Experimental source: cortex

A:Gene: elk2

C:Keywords: potassium channel

Alignment Scores:

Pred. No.: 9.43e-274

Score: 5428.00

Percent Similarity: 96.60%

Best local Similarity: 95.58%

Query Match: 89.14%

DB: 2

US-09-965-830-1-copy_6_3257 (1-3252) x T31100 (1-1087)

QY	1	ATGCCGGCCATGCGGGGCTCTGCGGCTCAGAACCTTCCTGACACATGCTACG	60
DB	1	MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CGCTTCACGCGACGACAGTACTTCGCTGCGGCAAGCGCGGCGGCGCTTC	120
DB	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlnValAlaGlyLeuPhe	40

[illegible]

RESULT 2
T17367

J. Physiol. 511, 675-682, 1998

A:Title: Cloning of a mammalian elk potassium channel gene and EMG mRNA distributed

A:Reference number: Z18731, M0ID:98382545, PMID:9714851

A:Accession: T17367

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-1102 <SH>

A:Cross-references: EMBL:AF061957; NID:93659689; PID:93659690; PIDN:AC61520.1

C:Gene: elk1

C:Function:

A:Description: may play a role in the sympathetic nervous system

C:Keywords: potassium channel

Alignment Scores:

Pred. No.:	6.98e-123	Length:	1102
Score:	2515.00	Matches:	551
Percent Similarity:	62.00%	Conservative:	149
Best Local Similarity:	48.80%	Mismatches:	295
Query Match:	41.30%	Indels:	134
DB:	2	Gaps:	24

US-09-965-830-1.COPY_6_3257 (1-3252) x T17367 (1-1102)

QY 1 ATGGCGGCGATCGGGGCGCTCTGCGGCGCTCAGAACACCTTCTGGACACACATCGCTAG 60

DB 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGCTTCAGAGGCGACGACAGTAACTTCTGCTGGGCAACGCCAGGTGGGGGCTCTTC 120

DB 21 ArgPheAspLysThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40

QY 121 CCCGTGCTACAGCTCTGTGATGGCTTCTGTACCTCAGCGGCTCTCCGGGCTGATGTC 180

DB 41 ProIleValLysThrSerAsnGlyPheCysGlyLeuLeuAlaGlyPheAlaArgThrGluVal 60

QY 181 ATGCACGGGGGCTGTGCTCTCTCTCTCTTTATGGGCGACAGCACCATGAGCTGCTCCG 240

DB 61 MetGlnLysSerCysSerCysLysPheLeuPheIleValGlnThrAsnGlnLeuMet 80

QY 241 CACAGATCCGACAGGCGCTTGACGACACAGGAGTCAAGCTGAGCTGATCTCTGAC 300

DB 81 LeuGlnIleGlnLysSerLeuGlnGlyLysValGlnPheLysGlyIleMetPheThr 100

QY 301 CGGAGAGCGGGCTCCGCTTGTGCTCTCTGATGATGATACCATTAAGATGAGAAA 360

DB 101 LysLysAsnGlyAlaProPheThrPheCysLeuLeuAspIleValProIleLysAsnGlyLys 120

QY 361 GGGGAGTGGGCT 417

DB 121 GlyAspAlaValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140

QY 418 GGGGGCCCGACAGATGGAAGAGACAGGTGGTGGCGGCGCGATGATGGCGGACGA 477

DB 141 ThrSerGlnAspLysLysGlyAspArgAlaLysGlyArgSerArgAlaIle----- 157

QY 478 TCCAAAGGCTTCATAGCCACCGGGGGGAGCCGGCGGCTCTCTCTCTCTCTCTCTCTCT 537

DB 158 ---SerHisPheAspSerAlaArgArgSerArgAlaValLeuThrHisLysSerGly 176

QY 538 CACCTGCAGAGACGCCCAAGGAGGACAGACAGTCAATTAAGGGGCTGTTGGGAGAA 597

DB 177 HisLeuGlnArgArgGlyLysAsnLysLeuLysIleAsnAsnValPheValAspLys 196

QY 598 CCAAACTTGCTTGAAGTAAAGTACGCCCATCGGAGCGCCCTTATCTCTGTTGAC 657

DB 197 ProAlaPheProLysLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216

QY 658 TGTGGGCGACTGAGACCACTGGGATGGCTTCACTCTCTCTCTCTCTCTCTCTCTCTCT 717

DB 217 PheSerThrPheLysIleGlyTrpAspThrPheLeuIleLeuLeuAlaThrPheThrValAla 236

718 GTCACGTGTCCT

D	569	ThSerPheCysAlaProGlyGlnTrpLeuAlaGlnGlyAlaLeuGlnAlaLeu	588
O	1858	TACTTTGTCCTTGGCTCATGGAGGTGCTCAAGGCTGGACCGCTGCTGCCATCTA	1917
D	589	TyrPheValCysSerGlySerMetGluValLeuAlaAspSerMetValLeuAlaLeu	608
O	1918	GGGAGGGCGACGATCGGCTGTGAGCTGCCCCGGCGGAGCAGCTGCTAAAGCCAT	1977
D	609	GlyValGlyAspLeuIleGlyAlaAsnLeuSerIleLysAspIleValIleLysThrAsn	628
O	1978	GCCGACGTGAAGGGGCTGACACTGCTGCTCTGCACTGCTGTGACAGTGGTGGCCCTGAC	2037
D	629	AlaAspValLysAlaLeuThrTrpCysAspLeuGlnCysIleIleLeuLysGlyLeuPhe	648
O	2038	GACACGCTTGGCTGATCCCGAATTGGCCCCGGCGGCTGACTGCTGAGCTCCGAGGGAG	2097
D	649	GluValIleGlyLeuTrpProGlyTrpAlaHisLysPheValGluAspIleGlnHisAsp	668
O	2098	CTCCACTACACCTGGGTCTGGG-----GGAGCTCT	2130
D	669	LeuThrTrpAsnLeuArgIleGlyHisIleGlnSerAspValIleSerArgLeuSerAsnLys	688
O	2131	GCAAGGTGACACGACGCTCCCTGAGCGCGACATACCTTATGTCACGCTG-----	2184
D	689	SerThrValProGlnAlaGluProLysGlyAsnGlySerIleLysArgLeuProSer	708
O	2185	-----GAGAGAGAAGACAGATGGGGAGCAGGGCCCCAGGCTGTCCCGACGCCA	2235
D	709	IleValIleAspIleGlnIleGlnGluValGlnGlnGluGlnIleThrTrpSerLeuSerPro	728
O	2236	GCTGATGAGCCCTCCAGCCGCCCTGCTGCTCCCTGCTGACCTCCTCATCTCCAGCTGCC	2295
D	729	IleTrpThrArgLysSerValSerHisSerLysIleLysThrGlySerSerLysSerTrp	748
O	2296	AAGCTGTATCCCACTGCA-----ACAGCACC-----CGGCT-----CGT	2334
D	749	LeuGlyLeuSerLeuLysGlnLeuThrSerGlyThrValProPheHisSerProLeuArg	768
O	2335	CTAGGTGACAGAGGAGCCAGCAGGAGGGGCTTTGAAGCTGAGGCTGGCCCTCT	2394
D	769	ValSerSerAlaAsnSerPro-----LysThrLysGlnIleValAspProPro	784
O	2395	GCTCCCCACGGGCTCAG-----GGCTAGGCTGCCCCCGCCCATGCAAT	2445
D	785	AsnHisGlyThrArgLysGlnLysAsnLeuLysValGlnIleLysSerLeuGlyThrAla	804
O	2446	GTGCCCCAGATCTGAGCCCGAGGTGATGATGCATTGACAGCGCTGTGGCTGGAC	2505
D	805	GlyThrProGlnLeuSerProArgIleAlaAspIleGlnAspGlyLysSerSerGln	824
O	2506	CAGCCCAAG-----TTCCTTCCGCTGGGCGCATCTGGCCGGATGTACACACGCC	2562
D	825	GlyThrGlnThrPheAspPheGlySerGlnIleArgProGlnProArgIleSerPro	844
O	2563	TCCCTCGACACGAG-----AGCGGCTGCTCACTGTCCCATGGGCCGACGAG	2613
D	845	SerLeuGlyGluSerGlnIleGlyAlaAlaPheLeuPheIle-----Lys	859
O	2614	GCAAGACACA-----GACACACTGGACACAAGTGTGGCGGCTGACAGACTGTGACAG	2670
D	860	AlaGlnGlyThrLysGlnIleAsnLysLeuAsnSerGluValThrThrLeuThrGln	879
O	2671	CAGGTGCTGCAATGCGGGAGAGGATGCACTGATCTCCGACAGGCTGTGACGCTTGTCTG	2730
D	880	GluValSerIleLeuLysLysAspMetArgSerIleMetGlnLeuLeuGlnAsnIleLeu	899
O	2731	GCGCGCCACAGAGGAGGTCCGTCCCTCGCGCATCGGAGAGGGGCGCTGCCACGAC	2790
D	900	SerProGlnIleProSerGlnPheCysSerLeuHisProThrSerIleCysProSerArg	919
O	2791	ACCTCGCGGCTTGCAGCCTCTGTGTGTGACACTGGGGCATCTCTCACTAGCTGGAG	2850
D	920	GluSerPheGlnThrArg-----ValSerTrpSerAlaHisGlnProCysLeuHis	936

QY 2851 CCCGACGT-----GGCTGTCTTGAAGTGGAGCTGGCCAC 2889
 Db 937 LeuGlnAlaAsnGlyAlaHisLeuTyrHisGlyAsnValThrSerIleTyr-----954
 QY 2890 CCTGCTCCGGGCGCTCCCTCCATAGCACTGGCCCTGGGGTCCCGACGCTCTAG 2949
 Db 955 -----SerValAspProSerLeuValGlySerAsnProGlnAthrGlnAlaHisGlu 972
 QY 2950 AGCTCCGCC----- 2958
 Db 973 GlnSerProValAspSerGluLeuHisSerProAsnLeuAlaTyrSerProSerHis 992
 QY 2959 -----TGCGCTGAGCCACA 2973
 Db 993 CysGlnValIleGlnGluGlyHisLeuGlnPheLeuAlaGlyCysIleSerProHisSerasp 1012
 QY 2974 GCTTTGAGACCTCCACTCAGACTCAGAGCCCTGCTCAGAGAGAGAGCTGCTGAG 3033
 Db 1013 ThrThrLeuThrProLeuGlnSerIleSerAlaThrLeuSerSerSerValCysSerSer 1032
 QY 3034 CCCGACCCCT-----GCTCCCTCTCTCTCTGAGAGAGGGCTAGAGACT--- 3081
 Db 1033 SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGlnGlySerIleThrHis 1052
 QY 3082 GGGCCCGCAGAGCTGTGAGCCAGCTGAGGCTACAGACTGAGAGAGCCCGACAGAGG 3141
 Db 1053 GlyProValSerSerPheSerLeu-----GluAsnLeuProGly 1065
 QY 3142 TCAGGGGGCTGCGCTTGGCTGGGAC 3168
 Db 1066 Ser-----Trpasp 1068
 RESULT 3
 T31354
 probable potassium channel elk chain 1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T31354
 R:Engelard, B.; Neu, A.; Ludwig, J.; Roeper, J.; Pongs, O.
 A:Submitted to the EMBL Data Library, July 1998
 A:Description: Identification of three rat potassium channel genes homologous to D. melanogaster
 A:Reference number: 220983
 A:Accession: T31354
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1017 <EMBL>
 A:Cross-references: EMBL:AJ007628; NID:e1329997; PID:e1329998; PIDN:CA07587.1
 A:Experimental source: cortex
 C:Genetics:
 A:Gene: elk1
 C:Keywords: potassium channel
 Alignment Scores:
 Pred. No.: 5.65e-119 Length: 1017
 Score: 2439.50 Matches: 532
 Percent Similarity: 60.00% Conservative: 131
 Best Local Similarity: 48.14% Mismatches: 244
 Query Match: 40.06% Indels: 198
 Gaps: 23
 US-09-965-830-1_COPY_6_3257 (1-3252) x T31354 (1-1017)
 QY 1 ATGCGCGCATGCGGCGCTCTGCGCTTGAACAACCTTCTGAGACCATGCTGACG 60
 Db 1 MelProValMetGlyGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTACAGCGAGCAGCACTGCTGCTGAGCAAGCCAGCGGCGGCTCTTC 120
 Db 21 ArgPheAspGlyThrHisSerAsnPheLeuAlaAsnAlaGlnGlyProArgGlyPhe 40
 QY 121 CCGGTGCTACTGCTCTGATGCTTCTGAGCTCAGGGGCTTCCCGGCTGAGCTC 180
 Db 121 ----- 180

Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuThrGlyTyrGlyArgThrGluVal 60
 QY 181 ATCAGCGGGGCTGTGGCT 240
 Db 61 MetGlnHisThrCysSerCysArgPheLeuTyrGlyProGluThrSerGluProAlaLeu 80
 QY 241 CAACAGATCCGCAAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 Db 81 GlnArgLeuGlnValAlaLeuGlnGlyHisGlnGlnHisArgAlaGlnIleCysPheTyr 100
 QY 301 CGAGAGAGGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 Db 101 ArgGlyAspGlySerAlaThrPheTyrCysLeuAsnMetPheProIleCysAsnGluLeu 120
 QY 361 GGGAGGAGGCT 420
 Db 121 GlyGluValValLeuPheLeuPheSerPheCysAspIleSerGlnSerGlyGlyProGly 140
 QY 421 -----GGCCCGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
 Db 141 LeuGlySerProGlyIleHisGlyAspAsnAsnHisGluAsnSerLeuGlyArg--- 159
 QY 460 CGATATGCGCGGCGAGCATCCAAAGCTTCAATGCCAACCGCGGCGAGCGCGCGCTG 519
 Db 160 -----ArgGlyAlaSerSerArgLeuArgSerThrArgArgGlnAsnArgThrVal 176
 QY 520 CTATACACCTGTCCGCGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 579
 Db 177 LeuHisArgLeuThrGlnHisPheGlyArgArgAspGlnGlySerValValAlaAsnSer 196
 QY 580 GGGGTGTTGGGAGAAACCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
 Db 197 AsnValPheGluProLysProSerValProGluTyrIleValAlaSerValGlyGlySer 216
 QY 640 CCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699
 Db 217 ArgCysLeuLeuLeuHisTyrSerIleProLysAlaValThrAspGlyLeuLeuLeu 236
 QY 700 GCCACACTATATGAGGTGACATGCGCTTACAGAGCTGTGTGAGACAGAGAGAGAG 759
 Db 237 AlaThrPheTyrValAlaValThrValProTyrAsnValAlaGlySerPheAlaGlyAspAsp 256
 QY 760 CCGAGTCCG 819
 Db 257 ThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPheIle 276
 QY 820 CTTGACATTTGCTGATATTCCTTACACATTCGCTTCCAAAGCGGGCGAGCGGTGTT 879
 Db 277 LeuAspIleIleLeuAsnPheArgThrThrTyrValSerGlnSerIleGlnValValSer 296
 QY 880 GCCCCAAATCCATTGCTCCCTCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 939
 Db 297 AlaProArgSerIleGlyLeuHisTyrLeuAlaIleThrPhePheValAspIleAla 316
 QY 940 GCGTGCCTTGTGACCTGTATAGCTTCAAGGTCAACGCTACTTCTGGGCCCATCTG 999
 Db 317 AlaLeuProPheAspLeuTyrValPheAsnIleThrValThrSerLeuValHisLeu 336
 QY 1000 CTGAAGAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1059
 Db 337 LeuTyrThrValArgLeuLeuArgLeuLeuArgLeuLeuGlnValGlnGluArgTyrSer 356
 QY 1060 CAGTACAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119
 Db 357 GlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHisTyr 376
 QY 1120 GTGCGCTGCTGCTGCTTTCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1179
 Db 377 MetAlaCysValTyrTyrValIleGlyArgArgGluMetGluAlaAsnAspProLeuLeu 396
 QY 1180 CCTAGATATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1239
 Db 397 TrpAspIleGlyTyrThrHisGlnLeuGlyLysArgGlnGluGluProTyr----- 413

QY 1240 GGGCGAGGCCAGCTGGAGGGAACAGCTCCGGCAGAGTGAACACTGCAGCAGCAGC 1299
 Db 413 ----- 413
 QY 1300 GAGGCCAAGGGAGGGGGTGGAGTGTGGGCGCCCTGCTGGCAGCGCTTACATC 1359
 Db 414 ---ValAsnGlySerIle-----GlyGlyProSerArgArgSerAlaTyrIle 428
 QY 1360 ACCCTCCCTACTTCCGACACTCAGACCCCTCACCAGCGTGGGCTTGGCAACGTGTCGCC 1419
 Db 429 AlaIleLeuTyrPheThrIleuSerSerIleuThrSerValGlyPheGlyAsnValCysAla 448
 QY 1420 AACAGGACACCCAGAGAGATCTTCTCATGTGCACCATGTGCATGGCGCCGATGCAC 1479
 Db 449 AsnThrAspAlaGlyIleuSerIleCysThrMetLeuIleGlyAlaLeuMetHis 468
 QY 1480 GCGGTGTGTGGGAACGTGACGGCGCCATCCAGCGCATGACGCCCGCTTCTG 1539
 Db 469 AlaValAlaPheGlyAsnValThrAlaIleIleGlyMetIleTyrSerArgArgSerLeu 488
 QY 1540 TACCAACGCGGCAAGCGGACCTGCGACATCCGACATCCGACATCCGATCCCAAGCC 1599
 Db 489 TyrIleSerArgMetLysAspLeuLysAspPheIleArgValHisArgLeuProArgPro 508
 QY 1600 CTTAAGAGGCGCATGTGAGTACTTCCAGGSCACCTGGCGGTGACATGCAATGCATGCAC 1659
 Db 509 LeuLysGlnArgMetLeuGlyIleTyrPheGlnThrThrAlaValAsnSerGlyIleAsp 528
 QY 1660 ACCACCGAGTGTGACAGAGCTCCCTGACAGAGCTGGCGCGGACAGACATGCCATGCCTG 1719
 Db 529 AlaAsnGlnLeuLeuArgAspPheProAspGlnLeuArgAlaAspIleAlaMetHisLeu 548
 QY 1720 CACAAGAGGCTCTCCACCTGSCCATCTGTTGAGCGGCGGACCGGCGCTTCCGCGCA 1779
 Db 549 AsnArgGlnIleLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArgAla 568
 QY 1780 CTGTCTGTGGCGCCGCGCGCCCTTGCACGCGGCGGAGTACCTCATCCACCAAGCC 1839
 Db 569 LeuSerLeuHisIleLeuThrSerPheCysAlaProGlnLeuPheLeuArgArgGly 588
 QY 1840 GATGCGCTCAGAGGCTTACTTGTCTGTCTGCTGCTCATGAGAGTGTCTCAAGGTGGC 1899
 Db 589 AspAlaLeuGlnAlaHisIleTyrValCysSerGlySerLeuGlnValLeuArgAspAsn 608
 QY 1900 ACCCTCTCCGACATCTCAGAGAGGCGGACCTGATGCGCTGAGCTGAGCGCGCGGAG 1959
 Db 609 ThrValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspIleProGlnLeuGly 628
 QY 1960 CAG-----GTGGTAAGGCCAATGCCAGCTGAGAGGGGCTG 1995
 Db 629 GlnGlnProGlnAlaGlyAlaGlyCysValLeuLysThrSerAlaAspValLysAlaLeu 648
 QY 1996 AGCTACTGCTCTGCAAGTGTGCAAGCTGCTGCTGCAAGCAAGCTTGGCTGTAC 2055
 Db 649 ThrTyrCysGlyLeuGlnGlnLeuSerSerArgGlyLeuAlaGlnValLeuArgLeuTyr 668
 QY 2056 CCGGAGTGGCCCGCGCTCAGTCTGCGCTCCGAGGAGGAGCTCAGCTCAACAGTGGGT 2115
 Db 669 ProGlnTyrValAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPheAsnLeuArg 688
 QY 2116 GCTGGGGA-----GGCTTCGCA 2133
 Db 689 GlnGlySerGlnAsnAsnGlyLeuGlyArgPheSerArgSerProArgLeuSerGlnAla 708
 QY 2134 GAGGTGACACCCAGCTCCGAGCGGAGCAATCCCTTATGTCACGCTGAGAGAGAG 2193
 Db 709 ArgSerAspThrLeuGlnArgSerSerAspLysThrLeuProSerIle-----Thr 725
 QY 2194 GAGACAGATGGGAGCAGAGGCGCCACAGGCTTCCCGACCCAGCTGATGAGCCCTCCAGC 2253
 Db 726 GlnThrGlnGly-----GlyMetGlnProGlnAlaGlySerLysProArgArg 741

QY 2254 CCGCTGCTCCCTGGCTGACACCTCTCATCTCATCTGACATGCCAAGCTG----- 2301
 Db 742 ProLeuLeuLeuProAsnLeuSerProAlaArgProArgGlySerLeuValSerLeuLeu 761
 QY 2302 -----CTATCCCGCACGTGCA 2316
 Db 762 GlyGlnGlnLeuProPheSerAlaLeuValSerSerProSerLeuSerPro----- 779
 QY 2317 ACAGACACCCCGGCTGCTCAGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGCTTTGAG 2376
 Db 780 ---ThrProSerProAlaLeuAlaGlyArgGly----- 789
 QY 2377 GCTGAGGCTGGCCCTCT-----GCTCCCGCACGGGCGCTTACAGGGG----- 2418
 Db 790 ---SerSerProSerLeuHisGlyProProArgGlySerAlaAlaTyrLysProPro 807
 QY 2419 ---CTACGCTGCCCGCCCGACATGAGATGTGCCCGCCAGATCTGACCCCGAGGTAGTA 2475
 Db 808 GlnLeuLeuThrProProLeuGlnGlyThrPheGlyProProAspLeuSerProTyrIleVal 827
 QY 2476 GATGCATTTGAAGAGCGCTGTGC---TCGACACCAAGCCCAAGTCTCTTCCGGGTGGC 2532
 Db 828 AspGlyIleGlnAspSerSerAsnThrAlaGlnAlaProThrPheArgPhe----- 844
 QY 2533 CAGTCTGCGCCGGAATGTAGCAGACAGCCCTCCCTGAGCCAGAGAGCGGCTGCTCACT 2592
 Db 845 SerLysArgProGlnProThrArgThrArgSerGlnAlaProLeuSer----- 860
 QY 2593 GTTCCCGATGGGCGCCAGGAGGAGCAGAGAAC-----ACAGACACACTGACAGAGTTGCG 2646
 Db 861 -----GlyProArgLeuSerArgGlnLeuAlaThrGlnAlaAlaGlnGlnValLys 877
 QY 2647 CAGCGGTGACAGACCTGTGACAGAGGTGTGACAGATGCGGGAAGACACTGCAGTCACTT 2706
 Db 878 GlnLysValCysArgLeuAsnGlnGlnIleSerArgLeuAsnGlnGlnValSerGlnLeu 897
 QY 2707 CGCCAGGCTGTGACAGTCTTCTCTGGCGCCCGACAGAGAGGTCCGTGGCTGGGCGATCG 2766
 Db 898 SerArgGlnLeuArgGlnValMet----- 905
 QY 2767 GAGAGAGGCGCGTCCAGCAGACACCTCCGGGCTTGCAGAGCTGTGTGTGACACT 2826
 Db 906 -----GlyLeuLeuGlnAlaArg----- 911
 QY 2827 GGGGCACTCTCTACAGCTGCGTCCAGCCCGGAGGCTGTGTGATGAGTGGACTGGCCC 2886
 Db 912 -----LeuGlyProProSer----- 916
 QY 2887 CACCTCTGTCGGGCGCTCTCTCCCTCATGAGCACCTGCGCTGGGAGTCCCGCAGGCTCT 2946
 Db 917 HisPro-----ProAsp-SerThrThrLeuProAspLeuProCysProHis----- 931
 QY 2947 CAGAGCTCCCGCTGGCTGAGCCACAGCCTTTCTGACCTCCACCTCAGACTCAGAGAG-- 3004
 Db 932 -GlnArgProProCysAlaSerProHisMetSerGlyProProProGlyLeuGlnAsnThr 951
 QY 3004 ----- 3004
 Db 951 rThrLeuAlaValAlaHisCysProAlaSerValGlyThrValGlnIleGlyAlaThrPr 971
 QY 3005 -----CCCTGCTCAGAGAGACTCTGCTGAGCCC 3036
 Db 971 oSerGlnLeuArgSerSerMetValProProPheProSerGlnProAspProLeuGlyPr 991
 QY 3037 AGCACCCCTGGCT 3049
 Db 991 oSerProValPro 995
 RESULT 4
 131168
 Probable potassium channel elk chain - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13168
 R:Warrick, J.W.; Ganetzky, B.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994
 A:Title: A family of potassium channel genes related to eag in Drosophila and mammals.
 A:Accession: A54953; MUID:94211879; PMID:8159766
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 11284 <MAR>
 A:Cross-references: EMBL:U04246; NID:9487735; PID:9487736; PIDN:AAA62472.1
 A:Gene: elk
 A:Cross-references: FlyBase:FBgn0011589
 A:Map position: 2R

Alignment Scores:
 Pred. No.: 4,44e-91 Length: 1284
 Score: 1901.00 Matches: 455
 Percent Similarity: 53.85% Conservative: 146
 Best Local Similarity: 40.77% Mismatches: 273
 Query Match: 31.22% Indels: 242
 DB: 2 Gaps: 31

US-09-965-830-1_COPY_6_3257 (1-3252) x T13168 (1-1284)

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QY 1 ATGCGGCGCATGCGGGCTCTCTGCGCGCTGCGAAGACCTTCCTGAGACCATGCTACG 60
DB 1 MetProAlaArgysglLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCAGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 120
DB 21 ArpPheAspGlyThrHisSerAsnPhelValLeuClValAsnAlaGlnValAsnGly 39
QY 121 CCGGTGCTACGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 40 ProIleValItyrCysSerAspGlyPheValAspLeuThrClYrSerAlaGlnIle 59
QY 181 ATGACGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 60 MetGlnIlyGlyCysSerCysHisPheLeuYrGlyProAspThrIlysglunHisLys 79
QY 241 CAACAGATCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
DB 80 GlnGlnIleGlnLysSerLeuSerAsnLysMetGlnLeuLysLeuValIlePheYr 99
QY 301 CGGAAGAGCGGCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 100 LysLysGlnGlyAlaProPheThrPysLeuPheAspIleValProIleLysAsnGln 119
QY 361 GGGGAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 411
DB 120 ArgAspValIlePheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGln 139
QY 411 ----- 411
DB 140 MetAsnValAsnGlnGlnCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGln 159
QY 412 -----AACGAGG 420
DB 160 ArgPheArgAlaGlySerAsnAlaGlnMetLeuGlnGlyGlyLeuProGlyLeuGly 179
QY 421 GGGCCC-----GACAGATGGAAGAGAGACAGTGGTGGCGCGCGCGCGCGCGCGCGCG 471
DB 180 GlyProAlaIleAspArgPheGlyAspThrGlnAlaGlnGlyGlnAsnAsnLeuAspValPro 199
QY 472 GCAGAGATCCAAAGGCTTCAATGCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 531
DB 200 Ala-----GlyCysAsnMetGlyArgArgArgSerArgAlaValLeuThrGlnLeu 216
QY 532 TCGGGGACCTGAGAGGACCCCAAGGCG-----AAGCACAAGCTCAATTAAGGCG----- 582
DB 217 SerGlnHisItyrLysProGlnLysGlyGlyValLysThrLysLeuLysLeuGlnAsn 236

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QY 583 ----GTGTTGGGAGAAACCAACTTGCCTGAGTACAAAGAGCCGACCTCCGAGCTCG 639
DB 237 PheMetHisSerThrGlnAlaProPheProGlnItyrLysThrGlnSerIleLysSer 256
QY 640 CCGTTATCTCTGTGACACTGTGGGCGACTGAGCGCCACTGGGAGCTTCATCTGCTGCT 659
DB 257 ArgLeuIleLeuProHisItyrGlyValPheLysGlyIleThrAspThrValIleLeuVal 276
QY 700 GCACACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
DB 277 AlaThrPheItyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg 296
QY 760 CCCAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 819
DB 297 GlnThr-----LysValSerAspValIleValGlnAlaLeuPheIle 310
QY 820 CTTGACATGCTGTAATTCCTGACACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 879
DB 311 ValAspIleLeuLeuAsnPhelArgThrThrPheValSerArgLysGlyValValValSer 330
QY 880 GCCCAAGGTCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
DB 331 AsnSerLysGlnIleAlaIleAsnItyrLeuArgGlyItyrPheAlaLeuAspLeuAla 350
QY 940 GCGGCGGCTTGCACCTCTACATGCTTCAAGTCAACGCTGCTGCTGCTGCTGCTGCTG 990
DB 351 AlaLeuProPheAsp-----HisLeuItyrAlaSerAspLeuItyrAspGlyLysSer 368
QY 991 ----GCCATGCTGGAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
DB 369 HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuGlnLysIle 388
QY 1048 GACCGTACTGCGAGTACAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1107
DB 389 AspArgItyrSerGlnHisItyrAlaMetIleLeuThrLeuMetPheSerPheThrLeu 408
QY 1108 CTGCGGCACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
DB 409 AlaAlaHisItyrLeuAlaCysIleItyrValIleAlaValLysGlyItyrGln----- 426
QY 1168 GAATCGAGTGGCTGAG-----ATTGCTGCTGCGAGAGCTGCGCGCGCGAG 1221
DB 427 -----TrpPheProGlnSerAsnIleGlyItyrLeuGlnLeuLeuAlaGlnArg----- 442
QY 1222 ACTCCCTACTACTGTTGGGCGCGGAGCGCACTGAGGAAACGCTCGGCGCAGAGTAC 1281
DB 442 ----- 442
QY 1282 AACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1341
DB 443 -----LysAsnAlaSerValAlaIleLeuThrAlaGln----- 454
QY 1342 CTGCGCAGCGCTATACATCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1401
DB 455 -----ThrLysSerThrAlaLeuItyrPheThrPheThrSerLeuThrValGly 471
QY 1402 TTGCGCAACGTTCGCGCAACGACGACGACGACGACGACGACGACGACGACGACGACG 1461
DB 472 PheGlyAsnValSerAlaAsnThrThrAlaGlnLysValPheThrIleLeuMetLeu 491
QY 1462 ATGCGCGCCGATGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
DB 492 IleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMet 511
QY 1522 TACGCGCGCCCTTCTCTTACACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1581
DB 512 TyrSerArgItyrSerItyrGlnSerItyrArgAspLeuLysAspPheValAlaLeu 531
QY 1582 CACCGTATCCCAAGCCCTTCAACAGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1641
DB 532 HisAsnMetProLysGlnLeuLysGlnArgIleGlnAspItyrPheGlnThrSerTrpSer 551
QY 1642 GTGAACAATGCGATCGACACCGAGCTGCTGAGAGCGCTCCCTGACGAGCTCGGCGCA 1701

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QY 757 GAGCCGAGTGC-----GCCCGCGCCCGCCGACGCTGTGACCTGGCC 8
 Db 439 GlyProAlaThrGlyGlyGlyTyrAlaGlyGlnProLeuAlaValValAspLeu 4
 QY 802 GTGAGAGCTCTTCATCCCTTGACATTTGGTGCGTAATTCGATACACATGCTGCACG 8
 Db 459 ValAspLeuMetHeuLeuValAspLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 4
 QY 862 TCGGCGCAGGTGGTGTGTGGCCCAAGTCCATTTGGCTCCACATGACACACTGGTTC 9
 Db 479 AsnGlnGlnValValSerHisProGlnArgGlnAlaValHisTyrPheLeuGlyTyrPhe 4
 QY 922 CTGCTGGATGTACATCCGACAGCTGGCTGGCTTTGACCTGTACATAGCTTCAAGCTAACCTG 9
 Db 499 LeuLeuAspMetValAlaAlaLeuPheProHisLeu----- 5
 QY 982 TACTTGGGGGCC-----CATCTGTGAAGACGTGGCTGCTGTGCG 1
 Db 512 IlePheGlySerGlySerGlnIleuLeuIleGlyLeuLeuLysThrAlaGlnLeuArg 5
 QY 1024 CTGCTGGCGCTGCTCTCCGCGGGGTGACCGGATCTCCAGATACAGCGCGCTGTGTACAA 10
 Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGlnTyrGlnAlaValLeuPhe 55
 QY 1084 CTGCTCATGGCGCGCTGTGGCTGGCTGCGGACAGCGGGTCCGCGTGTGTATCATTT 11
 Db 552 LeuLeuMetCysThrPheAlaLeuLeuIleAlaHisTyrLeuAlaCysIleTyrAlaIle 57
 QY 1144 GCGCCAGCGGGAGATCGACAGACGAGCAATCCGAGCTGAGATTGAGTGGCTGCAGGAG 12
 Db 572 GlyAsnMetGlnGlnProHisMetAspSer-----ArgIleLeuTyrLeuHisAsn 58
 QY 1204 CTGCGCGCGCGACAGCGAGACTCCCTTACTACTGTGTGGCGCGGACAGCTGGAGGAG 12
 Db 589 LeuGlnAspGlnIleGlyLysProTyr-----Asn 59
 QY 1264 AGCTCGCGCGAGATGACACACTCGACAGACAGACGAGCGGACGCGGGCTGGAG 13
 Db 599 SerSerLys----- 60
 QY 1324 CTGCTGGCGCGCGCTGCGCTGCGACAGCGCTACATACCTCCCTTACTTGGACATACG 13
 Db 602 ---LeuGlyGlnProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 62
 QY 1384 AGGCTACACAGAGTGGGCTTGGCAACAGTGTCCGCAACAGGACAGGACAGAAATGTTTC 14
 Db 621 SerLeuThrSerValGlnPheGlnAsnValSerProAsnThrAsnSerGlnLysIlePhe 64
 QY 1444 TCCATGTGACACATGTCTATCGCGCGCTGATGACAGCGGCTGTGTGGAGACGTGACG 15
 Db 641 SerIleCysValMetLeuLeuIleGlySerLeuMetTyrAlaSerIlePheGlnAsnValSer 66
 QY 1504 GGCATCATCAGCGCATGACACCGCGCGGCTTGTGATACACAGACCGCGAGCGAGCTG 15
 Db 661 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 68
 QY 1564 GCGGACATACATCCGACATCCAGCTATCCGCAAGCGCGCTCAAGACAGGCGATCTGGAGTAC 16
 Db 681 ArgGlnPheIleArgPheHisGlnIleProAsnProLeuArgGlnIleGlnGlnGlnTyr 70
 QY 1624 TTCCAGGCGCGACCTGGCGCGGTGAACATGAGCATGACACACAGAGTGGCGGACAGACCTTC 16
 Db 701 PheGlnHisAlaTyrSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 72
 QY 1684 CTTGACGAGTGGCGCGACATGCGGATGCGACCTGACACAGAGAGGCTCTGGAG---CTG 17
 Db 721 ProGlnCysLeuGlnAlaAspIleCysLeuHisIleuAsnArgSerLeuLeuGlnHisCys 74
 QY 1741 CCACTGTTTGAAGGCGCGACGCGGCGGTGCTGCGGCGACCTGTCTGGCTGCGGCGCC 18
 Db 741 LysProHeuArgGlnAlaThrLysGlyCysLeuArgGlnAlaLeuAlaMetLysPheLysThr 76

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Db 761 TThHisAlaProProGlyAspThrLeuValHisAlaGlySerLeuThrAlaLeuYr 780
1861 TTGTCTGCTCTGCTCCATGAGAGGTCTCAAGGTGGACCCGCTGCGCATCTTAAAGG 1920
781 PheIleSerArgGlySerIleGluIleLeuArgGlyAspValAlaValAlaIleLeuY 800
1921 AAGGGACCTGATCGGTGTGAGTGTCCCGGGGAGGAGGAGGTGAAGGCCAATGCC 1980
801 LysAsnAspIlePheGlyLeuProLeuAsnLeuYrAlaArgProGlyLysSerAsnGly 820
1961 GACGTGAGGGGGCTGACGTACGTGCTGCTGACGTGCTGACGTGCTGCTGCTGCTG 2040
821 AspValArgAlaLeuThrTyrcysAspLeuHisLysIleHisArgAspAspLeuLeuG 840
2041 AGCCTGCGCTTACCCGAGATTTGGCCCGCTTACGTGCTGCTGCTGCTGCTGCTG 2100
841 ValLeuAspMetLysProGlyPheSerAspHisPheTrpSerLeu-----GluIle 858
2101 ACCTACACCTG-----GGTCTGGGGGAGGAGCTCTGACAGAGGAGCAG 2142
859 ThrPheAsnLeuArgAspPheAsnMetIleProGlySerProGlySerThrGluLeuG 878
2143 ACCAGCTCCCTGACGGCGGACATATACCTTATGTCACGCTGAGAGAGAGAGACAGAT 2202
879 GlyGlyPheSerArgLysArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp 898
2203 GGGGACAGAGGGCCCAAGGCTCCCAAGCCCAAGCTGATGAGCCCTCCAGCCCTCTG 2262
899 ThrGluIle----- 901
2263 TCCCTGCTGCTGACCTCTGATCTGATCTGATGCTGATGCTGATGCTGATGCTGATG 2322
902 ---ProGlyGluValSerAla-----LeuGlyLysProGlyArgAlaGly 914
2323 CCCCAGCTCTGCTGATGCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2382
915 AlaGlyPro-----SerSerArgLysArgProGlyGlyProGlyGlyLysProSer 932
2383 GCTGCGCCCTCTGCTCCCA-----CGGCGCTTGAAGGGG 2418
933 SerGlyProSerSerProGlySerSerGlyAspGluGlyProGlyArgSerSerSerPro 952
2419 CTAGCGCTG-----CCCCCATGCGATGAAATGCCCCAGATCTGAGCCCC 2466
953 LeuArgLeuValProPheSerSerProArgProGlyGluProGlyGlyLysPro 972
2467 AGGAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2514
973 ---LeuMetGluAspCysGluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 991
2515 -----TTCCTTTC-----CGCGTGGGCGCATCT 2538
992 SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgLysArgLysGlu 1011
2539 GGGCGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2595
1012 LeuProArgCys-----ProAlaProThrProSerLeuLeuAsnIlePro 1026
2596 -----CCCATGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1042
1027 LeuSerSerProGlyArgArgProArgGlyAspValGluSerArg-----Leu 1042
2635 GACAGCTTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2691
1043 AspAlaLeuIleArgLysLeuAsnArgLeuGluIleThrArgLeuSerAlaAspMetAlaThr 1062
2692 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2751
1063 ValLeuGluIleLeuGluIleArgGluMetThrLeu----- 1073
2752 TGCCCTGGGCGATCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2811

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Db 1074 -----ValProProAlaTySerAla-- 1080
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2872 AGTGGAGCTTGGCCCCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2931
1099 Oleu-----ProThrLeuThrLeuAspSerLeuSerGln----- 1110
2932 GGTCCCGGAGCTCTC-----AGAGCTCCCGCTGAGGAGGAGGAGGAGGAGGAGGAG 2982
1111 -ValSerGlnPheMetAlaCysGluGluLeuProProGly---AlaProGluLeuProG 1129
2983 ACCTCCACCTGACACTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3042
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3043 CCGG 3046
1149 Oleu 1150

RESULT 6
A40853
potassium channel protein eag - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 10-Jul-1992 #sequence_rev1sion 10-Jul-1992 #text_change 24-Sep-1998
C:Accession: A40853
R:Winkler, J.; Drysdale, R.; Ganetzky, B.
Science 252, 1560-1562, 1991
A:Title: A distinct potassium channel polypeptide encoded by the Drosophila eag locus
A:Reference number: A40853; MIM:1262635; PMID:1840699
A:Accession: A40853
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1174 <VAR>
A:Cross-references: GB:M61157; NID:g157311; PID:g157312
A:Genetics:
A:Gene: FlyBase: eag
A:Cross-references: FlyBase: FBgn0000535
C:Keywords: transmembrane protein

Alignment Scores:
Pred. No.: 1,29e-64 Length: 1174
Score: 1390.00 Matches: 390
Percent Similarity: 47.57% Conservative: 198
Best Local Similarity: 31.55% Mismatches: 398
Query Match: 22.83% Indels: 250
DB: 2 Gaps: 42

US-09-965-830-1_COPY_6_3257 (1-3252) x A40853 (1-1174)
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1 MetProGlyGlyArgArgGlyLeuValAlaProGluAsnThrPheLeuGluAsnIleIle 20
58 AGCGGCTGACGAGGCG---ACGCACAGTAACTTGTGCTGAGGAGGAGGAGGAGGAGGAGG 114
21 ArgArgSerAsnSerGlnProAspSerSerPheLeuLeuAlaAsnIleGlnIleValAsp 40
115 CTGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 174
41 ---PheProIleValTyrcysAsnGluSerPheCysLysIleSerGlyTyrcysAlaAla 59
175 GAGTCATGACAGCGGGGCTG-----GCTGCTCTCTCTCTTATGGGCGGAGGAGGAGGAG 228
60 GluValMetGlnLysSerCysArgTyrcysValCysGlyPheMetTyrcysGluLeuThrAsp 79
229 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
80 LysGluThrValGlyArgLeuGluIleTyrcysLeuGluAsnGlnGlnAspGlnPheGlu 99
289 CTGATCTGATACCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 315

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[illegible]

Db 175 GlyIuAsnValIHisLysSerArgIeuAlaIValIleuGlnIleuGlySerAspIle 194
QY 586 TTTGGGGGAACCAACTTCCCTGAGTACAAAGTAGCCGACCTCCGAAAGTCCGCTTC 645
Db 195 -----LeuProGlnIleuLysGlnIleuAlaIleuProLysThrProHis 208
QY 646 ATCCGTTGACCTGGGGGACCTAGAGCCACTGGGATGGCTTCATCCTGCGCCACA 705
Db 209 IleIleuHisLysIleuValPheLysThrThrAspIleIleuIleuLeuThr 228
QY 706 CTCATGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Db 229 PheThrThrAlaIleuValProLysAsnValSerPheLysThr-----ArgGlnAsn 247
QY 766 GCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 825
Db 248 ValAlaIleu-----LeuValValAspSerIleValAspValIlePheLeuValAsp 264
QY 826 ATTTGCTGATTTCCGTACACATTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885
Db 265 IleValIleuAsnPheHisLysThrPheValGlyProAlaIleuValIleSerAspPro 284
QY 886 AAGTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
Db 285 LysLeuIleuArgMetAsnLysIleuLysThrThrPheValIleAspLeuLeuSerCysLeu 304
QY 946 CCGTTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 990
Db 305 ProLysAspValIleuAsnAlaPheGlnAsnValAspGlnGlyIleSerSerLeuPheSer 324
QY 991 GCGCATCTGCTGACAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1050
Db 325 Ser-----LeuLysValValArgLeuLeuArgLeuGlyArgValAlaArgLysLeuAsp 342
QY 1051 CGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1110
Db 343 HisLysIleuGlnLysIleuValAlaIleuValIleuLeuValCysValPheGlnLeuAla 362
QY 1111 GCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1170
Db 363 AlaHisThrPheAlaCysIleThrLysSerIleGlyAspLysGlnIlePheAspLysAsp 382
QY 1171 TCCGAG-----CTGCGTGAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1227
Db 383 ThrLysThrIleuArgAsnAsnSerThrLysGlnLeuAlaIleuAspIleLysThrPro 402
QY 1228 TACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1287
Db 403 TyrGlnPhe-----AsnGlySerGlySerGlyLysTrpGlu----- 414
QY 1288 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1347
Db 415 -----GlyGlyProSerLysAsn 420
QY 1348 AGCGCTACATACCTCCCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1407
Db 421 SerValLysIleuSerSerLysThrPheThrMetThrSerLeuThrSerValGlyPheLeu 440
QY 1408 AACGTGTCG 1467
Db 441 AsnIleuAlaProSerThrAspIleGlnLysIlePheAlaValAlaIleuMetIleGly 460
QY 1468 GCGCTGATGACGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1527
Db 461 SerLeuLeuLysThrAlaThrIlePheGlyAsnValThrThrIlePheGlnGlnMetLysAla 480
QY 1528 CCGCGCTTCTGCTGACACG 1587
Db 481 AsnThrAsnArgLysIleGlnMetLeuAsnSerValArgAspPheLeuLysLeuTrpGln 500
QY 1588 ATCCCAACCCCTCAAGACGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1647
Db 501 ValProLysGlyLeuSerGlnArgValMetAspLysIleValSerThrTrpSerMetSer 520

QY 1648 AATGCATGACACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1707
Db 521 ArgGlyIleAspThrGlnLysValLeuGlnIleCysProLysAspMetArgAlaAspIle 540
QY 1708 GGCATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1764
Db 541 CysValHisLeuAsnArgLysValPheLysGlnHisProAlaPheArgLeuAlaSerAsp 560
QY 1765 GCGTCCG 1824
Db 561 GlyLysLeuAlaGlnAlaLeuAlaMetGlnPheGlnThrValHisCysAlaProGlyAspLeu 580
QY 1825 CTCATCCACCAAGCGAGTCCCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1884
Db 581 IleThrHisAlaGlyLysSerValAspSerLeuLysPheValIleSerGlySerLeuGln 600
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Db 601 ValIleGlnAspAspGlnValValAlaIleLeuGlyLysGlyAspValPheGlyAspVal 620
QY 1945 CTGCG 2004
Db 621 PheThrLysGlnAlaThrIleuAlaGlnSerCysAlaAsnValArgAlaLeuThrTrpCys 640
QY 2005 GTCTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2064
Db 641 AspLeuHisValIleLysArgAspAlaLeuGlnLysValLeuGlnLysThrAlaPhe 660
QY 2065 GCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2109
Db 661 SerHisSerPheSerArgAsnLeu-----IleLeuThrLysLeuArgLysArgGly 678
QY 2109 ----- 2109
Db 679 ValPheArgLysIleSerAspValLysArgGlnGlnGlnLysArgLysAsn 698
QY 2109 ----- 2109
Db 699 GlnAlaProLeuIleuProProAsnHisProValArgArgLeuPheGlnArgPheArg 718
QY 2110 -----CTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2151
Db 719 GlnGlnLysGlnAlaArgLeuAlaIleuAlaGlnGlyLysArgAspLeuAspLeuAsp 738
QY 2152 CTGACCGCGGACAAATACCTTATGTC-----ACCTGAGAGAGAGAGAGAGAGAGAGAG 2208
Db 739 ValGlnLysGlyAsnAlaLeuThrAspHisLysSerAlaAsnHisSerLeuValLysAla 758
QY 2209 CAGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2268
Db 759 SerValValThrValArgLysSerProAlaThrProValSerPheGlnAlaAlaSer 777
QY 2269 GGTGCTACCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2328
Db 778 ---ThrSerThrValSerAspHisAlaLysLeuHisAlaProGlySerGlnCysLeuGly 796
QY 2329 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2367
Db 797 ProLysAlaGlyLysAspProAlaLysArgLysGlyTrpAlaArgPheLysAspAla 816
QY 2368 -----GCTTGAAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 817 CysGlyLysGlyLysAspTrpAsnLysValSerLysAlaGlnSerMetGlnThrLeuPro 836
QY 2401 CCAAGGCGCTAGAGGGGTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
Db 837 GlnArgThr-----LysAla 841
QY 2461 AGCCCCAGGGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
Db 842 SerGlyGlnAlaThrLeuLysLysThrAspSerCysAspSerGlyIleThrLysSerAsp 861

[illegible]

Yy 2221 GTCTCCCAAGCCCAAGCTGATGAGCCCTCCAGCCCCCTGCTGTCTGCTGAGCTGCC 2280
 Db 794 -----ProlethtrProvalSerPheGlnAlaIleThr 805
 Yy 2281 TCA-----TCCTAGCTGCCAAGCTG-----CTATCCCAAGT 2313
 Db 806 SerThrMetSerAspRnAlaLysLeuHnAlaProGlySerGlyLysLeuGlyProLys 825
 Yy 2314 CGAAGACA-----CCCGCGCCCTGCTAGT-----GGC 2343
 Db 826 AlaValSerGlyAspProAlaLysArgGlyGlyTrpAlaArgPheLysAspAlaCysGly 845
 Yy 2344 AGAGGAGGCCAGCAGGAGGAGGCGCTTTGAAGCTGAGGCTGAGCCCTGCTGCCCA 2403
 Db 846 LysGlyGlyLysPrrAsnLys---ValSerLysAlaGlySerMetGlyTrpLeuProGlu 864
 Yy 2404 CGGGCCCTAGAGGGGCTAGCGGCTGCCCCCATGCACTGGAAATGCCCCCAGATCTGAGC 2463
 Db 865 ArgThr-----LysAlaProGlyGluAlaThr 873
 Yy 2464 CCGAGGCTAGTAGATGGCATTTGAAGACGGCTGTGCTCGAGCAGCCCAAGTTCTTTTC 2523
 Db 874 LeuLysLysThr-----AspSerCysAspSerGlyIleThrLysSerAspLeu 889
 Yy 2524 CGCGTGGGCACTGTGCCCCGAAATGTAGCAGACAGCCCTCCCTGAGCAGAGAGCGGC 2583
 Db 890 ArgLeuAspAsnValGly-----GluThrArgSerProGlnAspArgSerPro 905
 Yy 2584 CTGCTCACT-----GTCCCATGGGCCAGCAGGAGCAAG 2619
 Db 906 IleLeuAlaGluValLysHnHisSerPheTyrProIleProGluGlnThrLeuGlnAlaThr 925
 Yy 2620 AACACAGACACACTGGACACAGCTTGGCAGGCGGAGACAGACAGCTGTACAGACAGTGTG 2679
 Db 926 ValLeuGluValLysTyrGluLeuLysGluAspIleLysAlaLeuAsnAlaLysMetThr 945
 Yy 2680 CAGATGCGGAGAGACTGCACTGCTGCCAGGCTGTGACAGCTTGAGCTGGCCGCCCCAC 2739
 Db 946 SerIleGluLysGlnLeuSerGlnIleLeuArg-----IleLeuMetSerArg 961
 Yy 2740 AGGAGGGTCCGCTGCCCTCGGCGCATCGGAGAGGAGGCGCTGCCAGCAGCAGC 2790
 Db 962 GlySerAlaGlnSerProGlnGluThrGlyGluLeuSerArgProGlnSer 978
 RESULT 9
 T42394
 potassium channel protein eag homolog - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence_rev1sion 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T42394
 R:Waterston, R.
 submitted to the EMBL Data Library, June 1999
 A:Reference number: Z22153
 A:Accession: T42394
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-934 <WAT>
 A:Cross-References: EMBL:AF036695; PIDN:AAB88348.1
 C:Genetics:
 A:Introns: 27/1; 66/2; 104/1; 147/1; 164/3; 222/2; 263/3; 301/3; 410/1; 468/2; 667/3
 A:Note: F16B3.1
 Alignment Scores:
 Score: 9.86e-58 Length: 934
 Pared. No.: 1257.00 Matches: 336
 Percent Similarity: 48.09% Conservative: 180
 Best Local Similarity: 31.31% Mismatches: 332
 Query Match: 20.64% Indels: 225
 DB: 2 Gaps: 33

05-09-965-830-1_COPY_6_3257 (1-3252) x T42394 (1-934)

[illegible]

[illegible]

us-09-965-830-1_copy_6_3257.rpr

[illegible]

Alignment Scores:		
Pred. No.:	1.43e-14	
Score:	423.50	Length: 735
Percent Similarity:	40.74%	Matches: 149
Best Local Similarity:	22.99%	Conservative: 115
Query Match:	6.96%	Mismatches: 224
DB:	2	Indels: 160
		Gaps: 22

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Db      487 rleuglllgiaglyserValphegylIvalSerValleuululeAlaAglyAsnArgTh 507
QY      1962 GGtGTAAAGGCCAATGCGACGCTGAAGGGGCTACGTACTGCCTCCTGACGTGTCA 2021
Db      507 rcllysnaAghAgtHrAlasInValArSlerLeugLYTysSeraspHeuCysLeuAl 527
QY      2022 GCTGGCTGGCCTCACGACGACCTTGCGGCTGTACCOCGAG 2061
Db      527 alysarGaspleurTpGlunThrleuSeraspTyrrProglu 540

RESULT 14
JC6509
rod cyclic nucleotide-gated cation channel protein alpha-chain - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #ext_change 21-Jul-2000
C:Accession: JC6509
R:Veske, A.; Nilsson, S.E.G.; Gal, A.
Gene 202, 115-119, 1997
A>Title: Characterization of canine rod photoreceptor cGMP-gated cation channel alpha
A:Reference number: JC6509; MUID:98087425; PMID:9427553
A:Accession: JC6509
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-691 <VS>
A:Cross-references: EMBL:X99914; NID:g1488571; PIDN:CA68186.1; PID:g1488572
C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotid
F:478-602/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CA
Alignment Scores:
Pred. No.:          1.81e-14          Length:           691
Score:              421.50            Matches:           145
Percent Similarity: 42.54%            Conservative:     126
Best Local Similarity: 22.76%         Mismatches:       265
Query Match:        6.92%             Indels:           101
DB:                2                  Gaps:            17

US-09-965-830-1_COPY_6_3257 (1-3252) x JC6509 (1-691)
QY      343 CCCATAAAGAATGGAAA-----GGGAGGTGGCTCTTCTCTCAACAAG 393
Db      74 ProSerGlnmrgrgluglnTYrleuproGlyAlaIleAlaIleAlaPheasnValnsnSer 93
QY      394 GACATCAGCGAAACCAAGAACCCAGGGGGCCCCGACAATGTAAGAGCACAGCTGTGCC 453
Db      94 SerAsnlysluglnngluProlysgluLylyslLylyslLylysgluLylysgluLylysglu 110
QY      454 CGGCGCCGATATGGCGGGGACGATCCAAAGCTTCATTGCACAGCGGGCGCGGACCGCG 513
Db      111 -----LysSerlySerClYaspLyssangluasnLylysllysnaspserrglu 125
QY      514 GCCGTCTCTACCACTGTCCGGGACCTGCAGAGCAGCCCAAGGGCAGACGACAAGCTC 573
Db      126 -----LysLylyslLylysgluLylysgluLylysgluLylysgluLylysglu 137
QY      574 AATTAAGGGGGTGTGGGGGAGAAACCAAACTTGCCTGAGTACAAAGTAGCGCATCCGG 633
Db      138 AsnLyslgluglnLylysglylsAspLylyslLylysgluLylysglu-----Lys 151
QY      634 AAGTGCCCTTCATCTGTGTGGGCACTGTGGGCACTGAGAGCGCACTGGAGTGGCTTCAATC 693
Db      152 LysglIvalMetValIleasproAlaAglyAsnmetTyrrAnsTrpleuphecysile 171
QY      694 CTGTCTCGCACACTGTATGTGGCTGTACACTGTGCCCTACAGCGGTGTGTGTAGACAGCA 753
Db      172 ThrleuproValMetTyrsanTrphmetyAlIleAlaArgalacySpheaspglueu 191
QY      754 CCGGAGCCCAAGTCCGCGCCGCGCGCGCCGCGCCAGCGTGTGTGACCTGCGCCGTGAGAGCTTC 813
Db      192 ginSeraspTyrrleuglnutyTrp-----lleIlePheaspTyrrleuSeraspIleVal 209
QY      814 TTCATCCCTTGACATGTGTGTAATTTCCGCTACCAACTTCGTGCCAAGTGGCGGACAGTG 873

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Db 210 TyrLeuLeuAspMetPheValArgThrArgThrGlyTyrLeuGlnGlyLeuVal 229
Qy 874 GTGTTTGGCCCAAGATTCATTCCTCCACTACGACCACTGGTCTCGTGGATGTC 933
Db 230 ArgGlnGlnAlaValLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 249
Qy 934 ATGGCAGCGCTGCGCTTGGACCTGCTACATCCCTCAAGGCAAC---GTGACTTGGG 990
Db 250 LeuSerValIleProThrAspLeuLeuTyr---PheLysLeuGlyTyrPheTyrProGlu 268
Qy 991 GCCCATGCTGTAAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1050
Db 269 IleArgLeuAsnArgLeuLeuValGlnIleSerArgMetPheGlnPheGlnArgThrGlu 288
Qy 1051 CGGATCTCGCATACAGCGCGTGGTG---CTGACACTGCTCATGCGCGTGGTGGCTG 1107
Db 289 ThrArgThrAsnTyrProAsnIlePheArgIleSerAsnLeuValMetTyrIleValIle 308
Qy 1108 CTCGCGACCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1167
Db 309 IleIleHisThrAsnAlaCysValTyrPheSerIleSerLysAlaIleGlyPheGlnLys 328
Qy 1168 GAATCCGAGCTG-----CCTGAGATTGGCTGGCTGCTGCTGCTGCTGCTGCTG 1209
Db 329 AspThrTyrValTyrTyrProAsnValAsnAspProGlnPheGly-----ArgLeuAla 345
Qy 1210 CGCGACCTGAGACTCCCTACTACTGCTGGGCGGAGCGGACGTGAGGAAACAGCTCC 1269
Db 346 ArgLys----- 347
Qy 1270 GGGCAGAGTGAACACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCTG 1329
Db 347 ----- 347
Qy 1330 GGGGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1389
Db 348 -----TyrValTyrSerLeuTyrTyrSerThrLeuThrLeu 359
Qy 1390 ACCAGCGTGGCTTGGGCACTGTCGCCCAACAGCGAAGAGTCTTCATC 1449
Db 360 ThrThrIleGly---GlnThrProProValArgAspSerGlnTyrValPheValVal 378
Qy 1450 TGCACCATCTCATCGGCGCGCGCGATGACAGCGGCTGTTGGACGTCAGCGGCATC 1509
Db 379 ValAspPheLeuIleGlyValLeuIlePheAlaThrIleValGlnLysIleGlySerMet 398
Qy 1510 ATCCACGCGATGACGCGCGCGCTTCTGTACACAGCGCGGCGGCGGACCTGCGGAC 1569
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Qy 1570 TACATCCGATCCACCGATCCCAAGCCCTCAGCAGCGCATGCTGGAGTACTTCAG 1629
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Qy 1630 GCCACCTGGCGGCTGAACAATGCGATCGACACACAGCGAGCTGCTGACAGACCTCCG 1689
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Qy 1690 GAGCTGCGGCAACATCGGCATGCGACCAAGAGGCTGCTG---CAGTGGCCACTG 1746
Db 459 LysLeuArgAlaGlnIleAlaIleAsnValHisLeuAspThrLeuLysLysValArgIle 478
Qy 1747 TTTGAGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1806
Db 479 PheAlaAspCysGlnAlaGlyLeuLeuValGlnIleValLeuLysLeuGlnProGlnVal 498
Qy 1807 TGCACGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1866
Db 499 TyrSerProGlnAspTyrIleCysLysLysLysLysLysLysLysLysLysLysLys 518
Qy 1867 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db 519 LysGlnGlnLysLeuAlaValAlaValAspAspGlyIleThrGlnPheValIleLeuSer 538

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Qy 1921 AAGGCGACCTGATCGC-----TGACGCTGCCCGCGGAGAGAGGTGTA 1968
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Qy 1969 AAGCCAAATCCCGGAGGAGGCGGCTGACGACGCTGCTGCTGCTGCTGCTGCTGCT 2028
Db 559 ArgArgThrAlaAsnIleLysSerIleGlyTyrSerAspLeuPheCysLeuSerLysAsp 578
Qy 2029 GGCCTGACGACGACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2088
Db 579 AspLeuMetGlnAlaLeuThrGlnTyrProAsp-----AlaLysThrMet 593
Qy 2089 CGAGGAGAGCTACCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2148
Db 594 LeuGlnGlnLysGlnLysGlnIleLeuMetLysAspGlyLeuLeuAsnIleAla 613
Qy 2149 TCCCTGACGCGGCGGACATACCTTATGCTGACGCTGAGGAGGAGGAGGAGACA 2199
Db 614 AsnAlaGlySerAsp-----ProLysAspLeuGlnGlnLysValThr 627

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RESULT 15

S74179

cyclic nucleotide-gated channel protein - human

C:Species: Homo sapiens (man)

C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999

C:Accession: S74179

R:Yu, W.P.; Grunwald, M.E.; Yau, K.W.

FEBS Lett. 393, 211-215, 1996

A:Title: Molecular cloning, functional expression and chromosomal localization of a h

A:Reference number: S74179; MUID:96409310; PMID:8814292

A:Accession: S74179

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-695 <YUW>

A:Experimental source: retina

C:Genetics:

A:Map position: 2

C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleot

C:Keywords: ion channel; ion transport; membrane protein

F:482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CA

Alignment Scores:

Pred. No.: 2,17e-14 Length: 695

Score: 420.00 Matches: 141

Percent Similarity: 42.25% Conserved: 96

Best Local Similarity: 25.13% Mismatches: 218

Query Match: 6.90% Indels: 106

DB: 2 Gaps: 17

US-09-965-830-1.copv_6_3257 (1-3252) x S74179 (1-695)

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Qy 787 GTCTGACCTGGCGCGGAGGTCCTTCATCTGACATTCGATTCGATTC 846
Db 205 ValLeuAspTyrSerAlaAspValLeuTyrValLeuAspValLeuValAlaGlnArgThr 224
Qy 847 ACATGCTGTCGAAGTGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
Db 225 GlyPheLeu---GlnGlnGlnLysMetValSerAspThrAsnArgLeuTyrGlnHisTyr 243
Qy 907 ---GTCAACACCTGGTTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 963
Db 244 LysThrThrThrGlnPheLysLeuAspValLeuSerLeuValProThrAspLeuAlaTyr 263
Qy 964 GCCTTCAAGTCAACGTGACTTGGGCGGCATGCTGTAAGAGCGGTGGCTGCTGCTGCTG 1023
Db 264 ---LeuLysValGlyThrAsnTyrProGlu-----ValArgPheAsnArgLeuLys 280
Qy 1024 CTGCTGCGCTGCTTCCGCGGCTGACCGGACTG----- 1059
Db 281 PheSerArgLeuPheGlnPhePheAspArgThrGlnThrArgThrAsnTyrProAsnMet 300
Qy 1060 ---CAGTACACGCGCGTGGCTGCTGACACTGCTCATGGCGCGTTCGCTGCGCGCAC 1116

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Db 301 PheArgIleGlyAsnLeuValLeuTyrIleLeu-----IleIleIleHis 315
OY 1117 TGGGTCGCTCGTGTGTTTACATGGCCAGGAGATCGAGAGACGCAATCCGAG 1176
Db 316 TrpAsnAlaCysIleTyrPheAlaIleSerIys-----PheIleHis 326
OY 1177 CTGGCTGAGATGGCTGCTGACAGAGCTGCGCCGACACAGACTCCCTACTACCTG 1236
Db 327 -----PheIleGlyPhe----- 330
OY 1237 GTGGGCGGAGGCGAGCTGGAGGACACCTCCGCGCAGACTGACAACTGGACAGCAGC 1296
Db 331 -----GlyThrAspSerThrPalaTyrProAsnIleSerIlePro 343
OY 1297 AGCGAGGCCAAGGAGGAGGAGGAGCTGAGACTGCTGGGCGCCGCTGCTGCGCAGCCTTAC 1356
Db 344 GluHisGlyArg-----LeuSerArgGlyTyr 352
OY 1357 ATGACCTCCCTTACTTCGACACACGACCTCAGCAGGCGGCGCTCCGCGCAGCTGCC 1416
Db 353 IleTyrSerLeuTyrIleTyrPheSerThrLeuThrIleGly---GluThrProPro 371
OY 1417 GCCAACAAGGAGACCGAGAGATCTTCATCTGCACATCCATCGAGCGGCGCTGATG 1476
Db 372 ProValIysAspGluGlyLeuPheValValAlaAspPheLeuValGlyValIle 391
OY 1477 CACGGGCTGTGTTGGGAAAGCTGACGACGATCATCGAGCGCATGTACGCCGCGCTT 1536
Db 392 PheAlaThrIleValGlyIleValGlySerMetIleSerAsnMetAlaSerArgAla 411
OY 1537 CTGTACACAGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1596
Db 412 GluPheGlnAlaIleValIleAspSerIleTyrGlnTyrMetGlnPheArgGlyValThrLys 431
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Db 472 ValHisLeuAspThrLeuLysValArgIlePheGlnAspCysGluAlaGlyLeuLeu 491
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OY 1834 CAAAGCGATGCGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1890
Db 512 LysGlyAspIleGlyLysGluMetTyrIleIleAsnGluGlyLysLeuAlaValAla 531
OY 1891 ---AAGGTGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1938
Db 532 AspAspGlyValThrGlnPheValValLeuSerAspGlySerTyrPheGlyGluIleSer 1938
OY 1939 ---TGTAGCTGCCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1995
Db 552 IleLeuAsnIleLysGlySerLysSerGlyAsnArgArgThrAlaAsnIleArgSerIle 571
OY 1996 ACGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2055
Db 572 GlyTyrSerAspLeuPheCysLeuSerLysAspAspLeuMetGluAlaLeuThrGluTyr 591
OY 2056 CCGGAGTTTGGCCGCGGCTTCAAGTGTGGGCTCCGAGGAGGAGCTCAAGCTCAACCTGGGT 2115
Db 592 ProGlyGlnAlaLysLys----- 597
OY 2116 GCTGGGGAGGCTCTGACAGACTGACACACAGCTCCCTGAGCGGCGGCGGCGGCGGCTTATG 2175

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Search completed: May 7, 2003, 15:24:20
 Job time : 186 secs

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Db 598 -----AlaLeuGluGluLysGlyArgGlnIleLeuMetLysAspAsnLeuIleAsp 614
OY 2176 TCCAGCTGAGAGAGAGAGACATGGGGAGAGAGGCGCCACGAGTCCCGGCGGCGGCGG 2235
Db 615 GluGluLeuAlaArgAlaGlyAlaAsp-----ProLysAsp 626
OY 2236 GCTGATGAGCCCTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2295
Db 627 LeuGluGluLysValGluGluLeuLysSerSerLeuAspThrLeuGlnThrArgPheAla 646
OY 2296 AAGCTGATATCCCAACGCTGCAACAGCACCC-----CGGCTGCTGCTA----- 2337
Db 647 ArgLeuAlaGluGlyArgAsnAlaThrGlnMetLysMetLysGlnArgLeuSerGlnLeu 666
OY 2338 -----GCTGGCAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2382
Db 667 GluSerGlnValLysGlyGlyLysAspLysProLeuAlaAspGlyGluValProGlyAsp 686
OY 2383 GCT 2385
Db 687 Ala 687

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